```
==============================================================
Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: Tue May 29 13:50:20 EDT 2007
==============================================================
```

Application No: 10578839   Version No: 1.0

                    Input Set:

                   Output Set:

                     Started: 2007-05-25 20:45:23.036
                    Finished: 2007-05-25 20:45:24.394
                     Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 358 ms
              Total Warnings: 10
                Total Errors: 0
        No. of SeqIDs Defined: 11
           Actual SeqID Count: 11

Error code   Error Description

W 213   Artificial or Unknown found in <213> in SEQ ID (1)

W 213   Artificial or Unknown found in <213> in SEQ ID (2)

W 213   Artificial or Unknown found in <213> in SEQ ID (3)

W 213   Artificial or Unknown found in <213> in SEQ ID (4)

W 213   Artificial or Unknown found in <213> in SEQ ID (5)

W 213   Artificial or Unknown found in <213> in SEQ ID (6)

W 213   Artificial or Unknown found in <213> in SEQ ID (8)

W 213   Artificial or Unknown found in <213> in SEQ ID (9)

W 213   Artificial or Unknown found in <213> in SEQ ID (10)

W 213   Artificial or Unknown found in <213> in SEQ ID (11)

SEQUENCE LISTINGS

<110>   INJE UNIVERSITY

<120>   CANCER CELL TARGETING GENE DELIVERY METHOD

<130>   Q94769

<140> 10578839
<141> 2007-05-25

<150>   US 10/578,839
<151>   2006-05-10

<150>   KR 10-2003-0079897
<151>   2003-11-12

<150>   PCT/KR2004/000545
<151>   2004-03-15

<160>   11

<170>   KopatentIn 1.71

<210>   1
<211>   36
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Env F primer

<400>   1
cgcggatccg aattccatac ctggtgttgc tgacta   36

<210>   2
<211>   47
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   597LN primer

<400>   2
agctggacct ggctgccacc acctccgcta ttttggtccc attttac   47

<210>   3
<211>   49
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   LC597 primer

<400>   3
caaccccgcc gcaggtggag gaggcagtga atggactcaa aaatttcaa   49

<210>   4
<211>   35
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Spike R2 primer

<400>   4
tgctctagaa ttcttaaagg ttaccttcgt tctct   35

<210>   5
<211>   36
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   LnkNScFv primer

<400>   5
ggaggtggtg gcagccaggt ccagctagtg cagtct   36

<210>   6
<211>   36
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   ScFvLnkC primer

<400>   6
actgcctcct ccacctgcgg cggggttgaa gtccca   36

<210>   7
<211>   2058
<212>   DNA
<213>   Gibbon Ape leukemia virus

<220>
<221>   sig_peptide
<222>   (1)..(126)

<220>
<221>   misc_feature
<222>   (127)..(1467)

<223>   surface subunit region

<220>
<221>   misc_feature
<222>   (1468)..(2025)
<223>   transmembrain domain

<400>   7
atggtattgc tgcctgggtc catgcttctc acctcaaacc tgcaccacct tcggcaccag   60

atgagtcctg ggagctggaa aagactgatc atcctcttaa gctgcgtatt cggcggcggc   120

gggacgagtc tgcaaaataa gaaccccac cagcccatga ccctcacttg gcaggtactg   180

tcccaaactg gagacgttgt ctgggataca aaggcagtcc agccccttg gacttggtgg   240

cccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccg   300

ggaaccgatg tctcgtcctc taaacgagtc agacctccgg actcagacta tactgccgct   360

tataagcaaa tcacctgggg agccataggg tgcagctacc ctcgggctag gactagaatg   420

gcaagctcta ccttctacgt atgtccccgg gatggccgga cccttcaga agctagaagg   480

tgcgggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt   540

tattggctat ctaaatcctc aaaagacctc ataactgtaa aatgggacca aaatagcgaa   600

tggactcaaa aatttcaaca gtgtcaccag accggctggt gtaaccccct taaaatagat   660

ttcacagaca aaggaaaatt atccaaggac tggataacgg gaaaaacctg gggattaaga   720

ttctatgtgt ctggacatcc aggcgtacag ttcaccattc gcttaaaaat caccaacatg   780

ccagctgtgg cagtaggtcc tgacctcgtc cttgtggaac aaggacctcc tagaacgtcc   840

ctcgctctcc cacctcctct tcccccaagg gaagcgccac cgccatctct ccccgactct   900

aactccacag ccctggcgac tagtgcacaa actcccacgg tgagaaaaac aattgttacc   960

ctaaacactc cgcctcccac cacaggcgac agactttttg atcttgtgca gggggccttc   1020

ctaaccttaa atgctaccaa cccaggggcc actgagtctt gctggctttg tttggccatg   1080

ggcccccctt attatgaagc aatagcctca tcaggagagg tcgcctactc caccgacctt   1140

gaccggtgcc gctgggggac ccaaggaaag ctcaccctca ctgaggtctc aggacacggg   1200

ttgtgcatag gaaaggtgcc ctttacccat cagcatctct gcaatcagac cctatccatc   1260

aattcctccg gagaccatca gtatctgctc ccctccaacc atagctggtg ggcttgcagc   1320

actggcctca ccccttgcct ctccacctca gttttttaatc agactagaga tttctgtatc   1380

caggtccagc tgattcctcg catctattac tatcctgaag aagttttgtt acaggcctat   1440

gacaattctc accccaggac taaaagagag gctgtctcac ttaccctagc tgttttactg   1500

gggttgggaa tcacggcggg aataggtact ggttcaactg ccttaattaa aggacctata   1560

gacctccagc aaggcctgac aagcctccag atcgccatag atgctgacct ccgggccctc   1620

caagactcag tcagcaagtt agaggactca ctgacttccc tgtccgaggt agtgctccaa   1680

aataggagag gccttgactt gctgtttcta aaagaaggtg gcctctgtgc ggccctaaag   1740

gaagagtgct gtttttacat agaccactca ggtgcagtac gggactccat gaaaaaactc   1800

aaagaaaaac tggataaaag acagttagag cgccagaaaa gccaaaactg gtatgaagga   1860

tggttcaata actccccttg gttcactacc ctgctatcaa ccatcgctgg gcccctatta   1920

ctcctccttc tgttgctcat cctcgggcca tgcatcatca ataagttagt tcaattcatc   1980

aatgatagga taagtgcagt taaaattctg gtccttagac aaaaatatca ggccctagag   2040

aacgaaggta acctttaa   2058

<210>   8
<211>   786
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Single-chain antibody Tag-72pS1 specific for Tag-72 surface
         antigen

<220>
<221>   misc_feature
<222>   (1)..(345)
<223>   heavy chain (H) variable region

<220>
<221>   misc_feature
<222>   (346)..(390)
<223>   (Gly4Ser)3 linker

<220>
<221>   misc_feature
<222>   (391)..(738)
<223>   light chain (L) variable region

<220>
<221>   misc_feature
<222>   (739)..(777)
<223>   PreS1 Tag

<220>
<221>   misc_feature

<400>   8
caggtccagc tagtgcagtc tggggctgaa gtgaagaagc ctggggcttc agtgaaggtg   60

tcctgcaagg cttctggcta caccttcact gaccatgcaa ttcactgggt gcgccaggcc   120

cctggacaac gccttgagtg gatgggatat tttctcctg gcaacgatga ttttaaatac   180

tcccagaagt tccagggacg cgtgacaatc actgcagaca atccgcgag cacagcctac   240

atggagctga gcagcctgag atctgaggac acggcggtct attactgtgc aagatcgttg   300

aacatggcat actggggcca agggactctg gtcactgtct cttcaggtgg aggcggttca   360

ggcggaggtg gctctggcgg tggcggatcg gacattgtga tgacccagtc tccagactcc   420

ctggctgtgt ctctgggcga gaggccacc atcaactgca gtccagcca gagtgtttta   480

tacagcagca acaataagaa ctacttagct tggtaccagc agaaaccagg acagcctcct   540

aagctgctca tttactgggc atctacccgg gaatccgggg tccctgaccg attcagtggc   600

agcgggtctg ggacagattt cactctcacc atcagcagcc tgcaggctga agatgtggca   660

gtttattact gtcagcaata ttattcctat ccgttgacgt tcggccaagg gaccaaggtg   720

gaaatcaaag cggccgcagg agccaacgca aacaatccag attgggactt caaccccgcc   780

gcatag   786

<210>   9
<211>   13
<212>   PRT
<213>   Artificial sequence

<220>
<223>   PreS1 epitope

<400>   9
Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro
  1   5   10

<210>   10
<211>   2871
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   ScFv-GaLV Env GP chimeric peptide (FvGEL199) DNA

<400>   10

atggtattgc tgcctgggtc catgcttctc acctcaaacc tgcaccacct tcggcaccag   60

atgagtcctg ggagctggaa aagactgatc atcctcttaa gctgcgtatt cggcggcggc   120

gggacgagtc tgcaaaataa gaaccccac cagcccatga ccctcacttg gcaggtactg   180

tcccaaactg gagacgttgt ctgggataca aaggcagtcc agccccttg gacttggtgg   240

cccacactta acctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccg   300

ggaaccgatg tctcgtcctc taaacgagtc agacctccgg actcagacta tactgccgct   360

tataagcaaa tcacctgggg agccataggg tgcagctacc ctcgggctag gactagaatg   420

gcaagctcta ccttctacgt atgtccccgg gatggccgga ccctttcaga agctagaagg   480

tgcgggggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt   540

tattggctat ctaaatcctc aaaagacctc ataactgtaa aatgggacca aaatagcgga   600

ggtggtggca gccaggtcca gctagtgcag tctggggctg aagtgaagaa gcctggggct   660

tcagtgaagg tgtcctgcaa ggcttctggc tacaccttca ctgaccatgc aattcactgg   720

gtgcgccagg cccctggaca cgccttgag tggatgggat attttctcc tggcaacgat   780

gattttaaat actcccagaa gttccaggga cgcgtgacaa tcactgcaga caaatccgcg   840

agcacagcct acatggagct gagcagcctg agatctgagg acacggcggt ctattactgt   900

gcaagatcgt tgaacatggc atactggggc caagggactc tggtcactgt ctcttcaggt   960

ggaggcggtt caggcggagg tggctctggc ggtggcggat cggacattgt gatgacccag   1020

tctccagact ccctggctgt gtctctgggc gagagggcca ccatcaactg caagtccagc   1080

cagagtgttt tatacagcag caacaataag aactacttag cttggtacca gcagaaacca   1140

ggacagcctc ctaagctgct catttactgg gcatctaccc gggaatccgg ggtccctgac   1200

cgattcagtg gcagcgggtc tgggacagat ttcactctca ccatcagcag cctgcaggct   1260

gaagatgtgg cagtttatta ctgtcagcaa tattattcct atccgttgac gttcggccaa   1320

gggaccaagg tggaaatcaa agcggccgca ggagccaacg caaacaatcc agattgggac   1380

ttcaacccccg ccgcaggtgg aggaggcagt gaatggactc aaaaatttca acagtgtcac   1440

cagaccggct ggtgtaaccc ccttaaaata gatttcacag acaaaggaaa attatccaag   1500

gactggataa cgggaaaaac ctggggatta agattctatg tgtctggaca tccaggcgta   1560

cagttcacca ttcgcttaaa aatcaccaac atgccagctg tggcagtagg tcctgacctc   1620

gtccttgtgg aacaaggacc tcctagaacg tccctcgctc tcccacctcc tcttccccca   1680

```
agggaagcgc accgccatc tctccccgac tctaactcca cagccctggc gactagtgca    1740

caaactccca cggtgagaaa aacaattgtt accctaaaca ctccgcctcc caccacaggc    1800

gacagacttt ttgatcttgt gcaggggggcc ttcctaacct taaatgctac caacccaggg    1860

gccactgagt cttgctggct ttgtttggcc atgggccccc cttattatga agcaatagcc    1920

tcatcaggag aggtcgccta ctccaccgac cttgaccggt ccgctgggg gacccaagga    1980

aagctcaccc tcactgaggt ctcaggacac gggttgtgca taggaaaggt gcccttacc    2040

catcagcatc tctgcaatca gaccctatcc atcaattcct ccggagacca tcagtatctg    2100

ctcccctcca accatagctg gtgggcttgc agcactggcc tcaccccttg cctctccacc    2160

tcagttttta atcagactag agatttctgt atccaggtcc agctgattcc tcgcatctat    2220

tactatcctg aagaagtttt gttacaggcc tatgacaatt ctcaccccag gactaaaaga    2280

gaggctgtct cacttaccct agctgtttta ctggggttgg aatcacggc gggaataggt    2340

actggttcaa ctgccttaat taaaggacct atagacctcc agcaaggcct gacaagcctc    2400

cagatcgcca tagatgctga cctccgggcc tccaagact cagtcagcaa gttagaggac    2460

tcactgactt ccctgtccga ggtagtgctc caaaatagga gaggccttga cttgctgttt    2520

ctaaaagaag gtggcctctg tgcggcccta aggaagagt gctgttttta catagaccac    2580

tcaggtgcag tacgggactc catgaaaaaa ctcaaagaaa aactggataa aagacagtta    2640

gagcgccaga aaagccaaaa ctggtatgaa ggatggttca taactcccc ttggttcact    2700

accctgctat caaccatcgc tgggcccta ttactcctcc ttctgttgct catcctcggg    2760

ccatgcatca tcaataagtt agttcaattc atcaatgata ggataagtgc agttaaaatt    2820

ctggtcctta gacaaaaata tcaggcccta gagaacgaag gtaaccttta a             2871


<210>      11
<211>      956
<212>      PRT
<213>      Artificial Sequence

<220>
<223>      ScFv-GaLV Env GP chimeric ligand (FvGEL199)


<400>      11
Met Val Leu Leu Pro Gly Ser Met Leu Leu Thr Ser Asn Leu His His
  1               5                  10                  15


Leu Arg His Gln Met Ser Pro Gly Ser Trp Lys Arg Leu Ile Ile Leu
              20                  25                  30
```

Leu Ser Cys Val Phe Gly Gly Gly Gly Thr Ser Leu Gln Asn Lys Asn
        35   40   45

Pro His Gln Pro Met Thr Leu Thr Trp Gln Val Leu Ser Gln Thr Gly
    50   55   60

Asp Val Val Trp Asp Thr Lys Ala Val Gln Pro Pro Trp Thr Trp Trp
65   70   75   80

Pro Thr Leu Lys Pro Asp Val Cys Ala Leu Ala Ala Ser Leu Glu Ser
            85   90   95

Trp Asp Ile Pro Gly Thr Asp Val Ser Ser Ser Lys Arg Val Arg Pro
            100   105   110

Pro Asp Ser Asp Tyr Thr Ala Ala Tyr Lys Gln Ile Thr Trp Gly Ala
        115   120   125

Ile Gly Cys Ser Tyr Pro Arg Ala Arg Thr Arg Met Ala Ser Ser Thr
    130   135   140

Phe Tyr Val Cys Pro Arg Asp Gly Arg Thr Leu Ser Glu Ala Arg Arg
145   150   155   160

Cys Gly Gly Leu Glu Ser Leu Tyr Cys Lys Glu Trp Asp Cys Glu Thr
            165   170   175

Thr Gly Thr Gly Tyr Trp Leu Ser Lys Ser Ser Lys Asp Leu Ile Thr
            180   185   190

Val Lys Trp Asp Gln Asn Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
    195   200   205

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
    210   215   220

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp
225   230   235   240

Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Phe Ser
            245   250   255

Pro Gly Asn Asp Asp Phe Lys Tyr Ser Gln Lys Phe Gln Gly Arg Val
            260   265   270

Thr Ile Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
    275   280   285

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu
    290   295   300

Asp Met Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
305   310   315   320

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
            325   330   335

Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg
        340   345   350

Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn
        355   360   365

Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
    370   375   380

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
385   390   395   400

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
            405   410   415

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr
        420   425   430

Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ala
        435   440   445

Ala Ala Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro Ala
    450   455   460

Ala Gly Gly Gly Gly Ser Glu Trp Thr Gln Lys Phe Gln Gln Cys His
465   470   475   480

Gln Thr Gly Trp Cys Asn Pro Leu Lys Ile Asp Phe Thr Asp Lys Gly
            485   490   495

Lys Leu Ser Lys Asp Trp Ile Thr Gly Lys Thr Trp Gly Leu Arg Phe
        500   505   510

Tyr Val Ser Gly His Pro Gly Val Gln Phe Thr Ile Arg Leu Lys Ile
        515   520   525

Thr Asn Met Pro Ala Val Ala Val Gly Pro Asp Leu Val Leu Val Glu
    530   535   540

Gln Gly Pro Pro Arg Thr Ser Leu Ala Leu Pro Pro Pro Leu Pro Pro
545   550   555   560

Arg Glu Ala Pro Pro Pro Ser Leu Pro Asp Ser Asn Ser Thr Ala Leu
            565   570   575

Ala Thr Ser Ala Gln Thr Pro Thr Val Arg Lys Thr Ile Val Thr Leu
        580   585   590

Asn Thr Pro Pro Pro Thr Thr Gly Asp Arg Leu Phe Asp Leu Val Gln
        595   600   605

Gly Ala Phe Leu Thr Leu Asn Ala Thr Asn Pro Gly Ala Thr Glu Ser
    610   615   620

Cys Trp Leu Cys Leu Ala Met Gly Pro Pro Tyr Tyr Glu Ala Ile Ala
625   630   635   640

Ser Ser Gly Glu Val Ala Tyr Ser Thr Asp Leu Asp Arg Cys Arg Trp
                645   650   655

Gly Thr Gln Gly Lys Leu Thr Leu Thr Glu Val Ser Gly His Gly Leu
                660   665   670

Cys Ile Gly Lys Val Pro Phe Thr His Gln His Leu Cys Asn Gln Thr
                675   680   685

Leu Ser Ile Asn Ser Ser Gly Asp His Gln Tyr Leu Leu Pro Ser Asn
690   695   700

His Ser Trp Trp Ala Cys Ser Thr Gly Leu Thr Pro Cys Leu Ser Thr
705   710   715   720

Ser Val Phe Asn Gln Thr Arg Asp Phe Cys Ile Gln Val Gln Leu Ile
                725   730   735

Pro Arg Ile Tyr Tyr Tyr Pro Glu Glu Val Leu Leu Gln Ala Tyr Asp
                740   745   750

Asn Ser His Pro Arg Thr Lys Arg Glu Ala Val Ser Leu Thr Leu Ala
                755   760   765

Val Leu Leu Gly Leu Gly Ile Thr Ala Gly Ile Gly Thr Gly Ser Thr
770   775   780

Ala Leu Ile Lys Gly Pro Ile Asp Leu Gln Gln Gly Leu Thr Ser Leu
785   790   795   800

Gln Ile Ala Ile Asp Ala Asp Leu Arg Ala Leu Gln Asp Ser Val Ser
                805   810   815

Lys Leu Glu Asp Ser Leu Thr Ser Leu Ser Glu Val Val Leu Gln Asn
                820   825   830

Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys Glu Gly Gly Leu Cys Ala
                835   840   845

Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ile Asp His Ser Gly Ala Val
        850   855   860

Arg Asp Ser Met Lys Lys Leu Lys Glu Lys Leu Asp Lys Arg Gln Leu
865   870   875   880

Glu Arg Gln Lys Ser Gln Asn Trp Tyr Glu Gly Trp Phe Asn Asn Ser
                885   890   895

Pro Trp Phe Thr Thr Leu Leu Ser Thr Ile Ala Gly Pro Leu Leu Leu
                900   905   910

Leu Leu Leu Leu Leu Ile Leu Gly Pro Cys Ile Ile Asn Lys Leu Val
                915   920   925

Gln Phe Ile Asn Asp Arg Ile Ser Ala Val Lys Ile Leu Val Leu Arg
        930   935   940

Gln Lys Tyr Gln Ala Leu Glu Asn Glu Gly Asn Leu
945   950   955